

SEQUENCE LISTING

<110> Old, Lloyd J.
Scanlan, Matthew J.
Chen, Yao-Tseng

<120> Cancer-Testis Antigens

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<150> US 60/280,718

<151> 2001-03-30

<150> US 60/285,154

<151> 2001-04-20

<150> US 60/327,432

<151> 2001-10-05

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<170> PatentIn version 3.1

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<212> PRT
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<400> 19

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20 25 30

Arg Ser Ile Ile Lys Glu Gly Ile Glu Ser Gln Ala Ser Tyr Lys Ile
35 40 45

Val Ile Glu Gly Lys Pro Tyr Thr Val Asn Leu Met Gln Lys Asn Phe
50 55 60

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Leu Pro His Asn Phe Arg Val Tyr Ser Tyr Ser Gly Thr Gly Ile Met
65 70 75 80

Lys Pro Leu Asp Gln Asp Phe Gln Asn Phe Cys His Tyr Gln Gly Tyr
85 90 95

Ile Glu Gly Tyr Pro Lys Ser Val Val Met Val Ser Thr Cys Thr Gly
100 105 110

Leu Arg Gly Val Leu Gln Phe Glu Asn Val Ser Tyr Gly Ile Glu Pro
115 120 125

Leu Glu Ser Ser Val Gly Phe Glu His Val Ile Tyr Gln Val Lys His
130 135 140

Lys Lys Ala Asp Val Ser Leu Tyr Asn Glu Lys Asp Ile Glu Ser Arg
145 150 155 160

Asp Leu Ser Phe Lys Leu Gln Ser Ala Glu Pro Gln Gln Asp Phe Ala
165 170 175

Lys Tyr Ile Glu Met His Val Ile Val Glu Lys Gln Leu Tyr Asn His
180 185 190

Met Gly Ser Asp Thr Thr Val Val Ala Gln Lys Val Phe Gln Leu Ile
195 200 205

Gly Leu Thr Asn Ala Ile Phe Val Ser Phe Asn Ile Thr Ile Ile Leu
210 215 220

Ser Ser Leu Glu Leu Trp Ile Asp Glu Asn Lys Ile Ala Thr Thr Gly
225 230 235 240

Glu Ala Asn Glu Leu Leu His Thr Phe Leu Arg Trp Lys Thr Ser Tyr
245 250 255

Leu Val Leu Arg Pro His Asp Val Ala Phe Leu Leu Val Tyr Arg Glu
260 265 270

Lys Ser Asn Tyr Val Gly Ala Thr Phe Gln Gly Lys Met Cys Asp Ala
275 280 285

Asn Tyr Ala Gly Gly Val Val Leu His Pro Arg Thr Ile Ser Leu Glu
290 295 300

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Ser Leu Ala Val Ile Leu Ala Gln Leu Leu Ser Leu Ser Met Gly Ile
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Thr Tyr Asp Asp Ile Asn Lys Cys Gln Cys Ser Gly Ala Val Cys Ile
325 330 335

Met Asn Pro Glu Ala Ile His Phe Ser Gly Val Lys Ile Phe Ser Asn
340 345 350

Cys Ser Phe Glu Asp Phe Ala His Phe Ile Ser Lys Gln Lys Ser Gln
355 360 365

Cys Leu His Asn Gln Pro Arg Leu Asp Pro Phe Phe Lys Gln Gln Ala
370 375 380

Val Cys Gly Asn Ala Lys Leu Glu Ala Gly Glu Glu Cys Asp Cys Gly
385 390 395 400

Thr Glu Gln Asp Cys Ala Leu Ile Gly Glu Thr Cys Cys Asp Ile Ala
405 410 415

Thr Cys Arg Phe Lys Ala Gly Ser Asn Cys Ala Glu Gly Pro Cys Cys
420 425 430

Glu Asn Cys Leu Phe Met Ser Lys Glu Arg Met Cys Arg Pro Ser Phe
435 440 445

Glu Glu Cys Asp Leu Pro Glu Tyr Cys Asn Gly Ser Ser Ala Ser Cys
450 455 460

Pro Glu Asn His Tyr Val Gln Thr Gly His Pro Cys Gly Leu Asn Gln
465 470 475 480

Trp Ile Cys Ile Asp Gly Val Cys Met Ser Gly Asp Lys Gln Cys Thr
485 490 495

Asp Thr Phe Gly Lys Glu Val Glu Phe Gly Pro Ser Glu Cys Tyr Ser
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His Leu Asn Ser Lys Thr Asp Val Ser Gly Asn Cys Gly Ile Ser Asp
515 520 525

Ser Gly Tyr Thr Gln Cys Glu Ala Asp Asn Leu Gln Cys Gly Lys Leu
530 535 540

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Ile Cys Lys Tyr Val Gly Lys Phe Leu Leu Gln Ile Pro Arg Ala Thr
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Ala Ser Asp His Ala Asp Ser Gln Lys Met Trp Ile Lys Asp Gly Thr
580 585 590

Ser Cys Gly Ser Asn Lys Val Cys Arg Asn Gln Arg Cys Val Ser Ser
595 600 605

Ser Tyr Leu Gly Tyr Asp Cys Thr Thr Asp Lys Cys Asn Asp Arg Gly
610 615 620

Val Cys Asn Asn Lys Lys His Cys His Cys Ser Ala Ser Tyr Leu Pro
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Pro Asp Cys Ser Val Gln Ser Asp Leu Trp Pro Gly Gly Ser Ile Asp
645 650 655

Ser Gly Asn Phe Pro Pro Val Ala Ile Pro Ala Arg Leu Pro Glu Arg
660 665 670

Arg Tyr Ile Glu Asn Ile Tyr His Ser Lys Pro Met Arg Trp Pro Phe
675 680 685

Phe Leu Phe Ile Pro Phe Phe Ile Ile Phe Cys Val Leu Ile Ala Ile
690 695 700

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725 730

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35 40 45

Thr Asp Val Glu Ala Phe Gln Gln Glu Leu Ala Leu Leu Lys Ile Glu
65 70 75 80

Asp Ala Pro Gly Asp Gly Pro Asp Val Arg Glu Gly Thr Leu Pro Thr
85 90 95

Phe Asp Pro Thr Lys Val Leu Glu Ala Gly Glu Gly Gln Leu
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 20 25 30

Asp Cys Asp Cys Phe Lys Glu Lys Ser Cys Pro Arg Leu Gly Tyr Gln
 35 40 45

Ala Lys Leu Phe Lys Gly Val Leu Lys Glu Arg Met Glu Gly Arg Pro
 50 55 60

Leu Arg Thr Thr Val Phe Leu Asp Thr Ser Gly Thr Tyr Pro Phe Cys
 65 70 75 80

Thr Tyr Tyr Phe Val Leu Ser Ile Ile Val Pro Asp Lys Thr Met Met
 85 90 95

Asp Gly Ser Phe Ser Phe Lys Leu Leu Asn Gln Leu Glu Met Ile Glu
 100 105 110

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Glu Pro Arg Leu Tyr Glu Lys Asn Lys Pro Phe Tyr Lys Leu Gln Glu
115 120 125

Val Lys Ile Leu Ala Gln Phe Tyr Asn Asp Phe Val Asn Ile Ser Ser
130 135 140

Ile Gly Leu Thr Tyr Phe Gln Ser Ser Asn Leu Gln Cys Ser Thr Cys
145 150 155 160

Thr Tyr Lys Ile Gln Ser Leu Met Leu Lys Ser Leu Thr Tyr Pro Glu
165 170 175

Arg Pro Pro Leu Cys Arg Tyr Asn Ile Val Leu Lys Glu Arg Glu Glu
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Val Phe Leu Asn Pro Asn Thr Cys Thr Pro Lys Asn Thr
195 200 205

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 <213> Homo sapiens

<400> 25

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20 25 30

Glu Val Asn Lys Leu Lys Glu Asp Leu Asn Glu Lys Thr Thr Glu Asn
35 40 45

Asn Glu Gln Arg Glu Glu Ile Ile Arg Leu Lys Gln Glu Lys Ser Cys
50 55 60

Leu His Asp Glu Leu Leu Phe Thr Val Glu Arg Glu Lys Arg Lys Asp
65 70 75 80

Glu Leu Leu Asn Ile Ala Lys Ser Lys Gln Glu Arg Thr Asn Ser Glu
85 90 95

Leu His Asn Leu Arg Gln Ile Tyr Val Lys Gln Gln Ser Asp Leu Gln
100 105 110

Phe Leu Asn Phe Asn Val Glu Asn Ser Gln Glu Leu Ile Gln Met Tyr
115 120 125

Asp Ser Lys Met Glu Glu Ser Lys Ala Leu Asp Ser Ser Arg Asp Met
130 135 140

Cys Leu Ser Asp Leu Glu Asn Asn His Pro Lys Val Asp Ile Lys Arg
145 150 155 160

Glu Lys Asn Gln Lys Ser Leu Phe Lys Asp Gln Lys Phe Glu Ala Met
165 170 175

Leu Val Gln Gln Asn Arg Ser Asp Lys Ser Ser Cys Asp Glu Cys Lys
180 185 190

Glu Lys Lys Gln Gln Ile Asp Thr Val Phe Gly Glu Lys Ser Val Ile
195 200 205

Thr Leu Ser Ser Ile Phe Thr Lys Asp Leu Val Glu Lys His Asn Leu
210 215 220

Pro Trp Ser Leu Gly Gly Lys Thr Gln Ile Glu Pro Glu Asn Lys Ile
225 230 235 240

Thr Leu Cys Lys Ile His Thr Lys Ser Pro Lys Cys His Gly Thr Gly
245 250 255

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Val Gln Asn Glu Gly Lys Gln Pro Ser Glu Thr Pro Thr Leu Ser Asp
260 265 270

Glu Lys Gln Trp His Asp Val Ser Val Tyr Leu Gly Leu Thr Asn Cys
275 280 285

Pro Ser Ser Lys His Pro Glu Lys Leu Asp Val Glu Cys Gln Asp Gln
290 295 300

Met Glu Arg Ser Glu Ile Ser Cys Cys Gln Lys Asn Glu Ala Cys Leu
305 310 315 320

Gly Glu Ser Gly Met Cys Asp Ser Lys Cys Cys His Pro Ser Asn Phe
325 330 335

Ile Ile Glu Ala Pro Gly His Met Ser Asp Val Glu Trp Met Ser Ile
340 345 350

Phe Lys Pro Ser Lys Met Gln Arg Ile Val Arg Leu Lys Ser Gly Cys
355 360 365

Thr Cys Ser Glu Ser Ile Cys Gly Thr Gln His Asp Ser Pro Ala Ser
370 375 380

Glu Leu Ile Ala Ile Gln Asp Ser His Ser Leu Gly Ser Ser Lys Ser
385 390 395 400

Ala Leu Arg Glu Asp Glu Thr Glu Ser Ser Ser Asn Lys Lys Asn Ser
405 410 415

Pro Thr Ser Leu Leu Ile Tyr Lys Asp Ala Pro Ala Phe Asn Glu Lys
420 425 430

Ala Ser Ile Val Leu Pro Ser Gln Asp Asp Phe Ser Pro Thr Ser Lys
435 440 445

Leu Gln Arg Leu Leu Ala Glu Ser Arg Gln Met Val Thr Asp Leu Glu
450 455 460

Leu Asn Thr Leu Leu Pro Ile Ser His Glu Asn Leu Thr Gly Ser Ala
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Thr Asn Ile Ser His Leu Cys Gly Arg Gln Lys Ala Asp Thr Asn Thr
485 490 495

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Glu

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20 25 30

Tyr Ser Ser Val Gln Val Pro Arg Arg Gly Ala Ile Leu Pro Met Leu

35

40

45

Tyr Ala Leu Cys Tyr Val Lys Met Pro Ser Phe Gln His Gly Pro Gly
50 55 60

Arg Met Tyr His Leu Thr Cys Asp Trp Pro Arg Lys Met Ser Leu Ser
65 70 75 80

Cys His Val Cys Arg Ala His Phe Arg Asp
85 90

<210> 28

<211> 2347

<212> DNA

<213> Homo sapiens

<400> 28

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ttgatgacct ctccatcccg ggtctgctgt ccaacacagg cctagtagcg cagctgggtc 660
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10054683 012300

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<210> 29
<211> 655
<212> PRT
<213> Homo sapiens

<400> 29

Met Ala Lys Gly Gly Glu Ala Leu Pro Gln Gly Ser Pro Ala Pro Val
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20 25 30

Glu Asp Phe Ser Val Thr Asp Thr Cys Thr Ile Gln Gln Leu Lys Glu
35 40 45

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Glu Ile Ser Gln Arg Phe Lys Ala His Pro Asp Gln Leu Val Leu Ile
50 55 60

Phe Ala Gly Lys Ile Leu Lys Asp Pro Asp Ser Leu Ala Gln Cys Gly
65 70 75 80

Val Arg Asp Gly Leu Thr Val His Leu Val Ile Lys Arg Gln His Arg
85 90 95

Ala Met Gly Asn Glu Cys Pro Ala Ala Ser Val Pro Thr Gln Gly Pro
100 105 110

Ser Pro Gly Ser Leu Pro Gln Pro Ser Ser Ile Tyr Pro Ala Asp Gly
115 120 125

Pro Pro Ala Phe Ser Leu Gly Leu Leu Thr Gly Leu Ser Arg Leu Gly
130 135 140

Leu Ala Tyr Arg Gly Phe Pro Asp Gln Pro Ser Ser Leu Met Arg Gln
145 150 155 160

His Val Ser Val Pro Glu Phe Val Thr Gln Leu Ile Asp Asp Pro Phe
165 170 175

Ile Pro Gly Leu Leu Ser Asn Thr Gly Leu Val Arg Gln Leu Val Leu
180 185 190

Asp Asn Pro His Met Gln Gln Leu Ile Gln His Asn Pro Glu Ile Gly
195 200 205

His Ile Leu Asn Asn Pro Glu Ile Met Arg Gln Thr Leu Glu Phe Leu
210 215 220

Arg Asn Pro Ala Met Met Gln Glu Met Ile Arg Ser Gln Asp Arg Val
225 230 235 240

Leu Ser Asn Leu Glu Ser Ile Pro Gly Gly Tyr Asn Val Leu Cys Thr
245 250 255

Met Tyr Thr Asp Ile Met Asp Pro Met Leu Asn Ala Val Gln Glu Gln
260 265 270

Phe Gly Gly Asn Pro Phe Ala Thr Ala Thr Thr Asp Asn Ala Thr Thr
275 280 285

10054633 01230

Thr Thr Ser Gln Pro Ser Arg Met Glu Asn Cys Asp Pro Leu Pro Asn
290 295 300

Pro Trp Thr Ser Thr His Gly Gly Ser Gly Ser Arg Gln Gly Arg Gln
305 310 315 320

Asp Gly Asp Gln Asp Ala Pro Asp Ile Arg Asn Arg Phe Pro Asn Phe
325 330 335

Leu Gly Ile Ile Arg Leu Tyr Asp Tyr Leu Gln Gln Leu His Glu Asn
340 345 350

Pro Gln Ser Leu Gly Thr Tyr Leu Gln Gly Thr Ala Ser Ala Leu Ser
355 360 365

Gln Ser Gln Glu Pro Pro Pro Ser Val Asn Arg Val Pro Pro Ser Ser
370 375 380

Pro Ser Ser Gln Glu Pro Gly Ser Gly Gln Pro Leu Pro Glu Glu Ser
385 390 395 400

Val Ala Ile Lys Gly Arg Ser Ser Cys Pro Ala Phe Leu Arg Tyr Pro
405 410 415

Thr Glu Asn Ser Thr Gly Gln Gly Gly Asp Gln Asp Gly Ala Gly Lys
420 425 430

Ser Ser Thr Gly His Ser Thr Asn Leu Pro Asp Leu Val Ser Gly Leu
435 440 445

Gly Asp Ser Ala Asn Arg Val Pro Phe Ala Pro Leu Ser Phe Ser Pro
450 455 460

Thr Ala Ala Ile Pro Gly Ile Pro Glu Pro Pro Trp Leu Pro Ser Pro
465 470 475 480

Ala Tyr Pro Arg Ser Leu Arg Pro Asp Gly Met Asn Pro Ala Pro Gln
485 490 495

Leu Gln Asp Glu Ile Gln Pro Gln Leu Pro Leu Leu Met His Leu Gln
500 505 510

Ala Ala Met Ala Asn Pro Arg Ala Leu Gln Ala Leu Arg Gln Ile Glu
515 520 525

100463 01200

Gln Gly Leu Gln Val Leu Ala Thr Glu Ala Pro Arg Leu Leu Leu Trp
530 535 540

Phe Met Pro Cys Leu Ala Gly Thr Gly Ser Val Ala Gly Gly Ile Glu
545 550 555 560

Ser Arg Glu Asp Pro Leu Met Ser Glu Asp Pro Leu Pro Asn Pro Pro
565 570 575

Pro Glu Val Phe Pro Ala Leu Asp Ser Ala Glu Leu Gly Phe Leu Ser
580 585 590

Pro Pro Phe Leu His Met Leu Gln Asp Leu Val Ser Thr Asn Pro Gln
595 600 605

Gln Leu Gln Pro Glu Ala His Phe Gln Val Gln Leu Glu Gln Leu Arg
610 615 620

Ser Met Gly Phe Leu Asn Arg Glu Ala Asn Leu Gln Ala Leu Ile Ala
625 630 635 640

Thr Gly Gly Asp Val Asp Ala Ala Val Glu Lys Leu Arg Gln Ser
645 650 655

<210> 30
<211> 899
<212> DNA
<213> Homo sapiens

<400> 30
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acaatgtcat ggctcggttac ctccctgcc aagtggagtt tgctgtccac acattcaacc 420
aacagagcaa ggactactat gcctacagac tggggcacat cttgaattcc tggaaggagc 480
aggtggagtc caagactgta ttctcaatgg agctactgct ggggagaact aggtgtggga 540
aatttgaaga cgacattgac aactgccatt tccaagaaag cacagagctg aacaatactt 600
tcacctgctt cttcaccatc agcaccaggc cctggatgac tcagttcagc ctctgaaca 660

agacctgctt ggagggattc cactgagtga aaccactca caggcttgctc catgtgctgc 720
 tcccacattc cgtggacatc agcactactc tcttgaggac tcttcagtgg ctgagcagct 780
 ttggacttgt ttgttatcct attttgcatg tgtttgagat ctcagatcag tgtttttagaa 840
 aatccacaca tcttgagcct aatcatgtag tgtagatcat taaacatcag cattttaag 899

<210> 31
 <211> 147
 <212> PRT
 <213> Homo sapiens

<400> 31

Met Leu Gly Leu Pro Trp Lys Gly Gly Leu Ser Trp Ala Leu Leu Leu
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Leu Leu Leu Gly Ser Gln Ile Leu Leu Ile Tyr Ala Trp His Phe His
 20 25 30

Glu Gln Arg Asp Cys Asp Glu His Asn Val Met Ala Arg Tyr Leu Pro
 35 40 45

Ala Thr Val Glu Phe Ala Val His Thr Phe Asn Gln Gln Ser Lys Asp
 50 55 60

Tyr Tyr Ala Tyr Arg Leu Gly His Ile Leu Asn Ser Trp Lys Glu Gln
 65 70 75 80

Val Glu Ser Lys Thr Val Phe Ser Met Glu Leu Leu Leu Gly Arg Thr
 85 90 95

Arg Cys Gly Lys Phe Glu Asp Asp Ile Asp Asn Cys His Phe Gln Glu
 100 105 110

Ser Thr Glu Leu Asn Asn Thr Phe Thr Cys Phe Phe Thr Ile Ser Thr
 115 120 125

Arg Pro Trp Met Thr Gln Phe Ser Leu Leu Asn Lys Thr Cys Leu Glu
 130 135 140

Gly Phe His
 145

<210> 32
 <211> 2186
 <212> DNA

00443 0346001

<213> Homo sapiens

<400> 32

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gcccaccctg gtgcgggagg cgacaggacc aggcctcgac ggcgccgttc cactgagagc	180
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agctcccaat attatgatgt gatgtattcc aagaaaggag ctgcctgggt gagtgagacg	600
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ataagagcca actttgatga ggttcaaagt ttccttctgc acttttggca aggaatgccg	840
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<210> 33
<211> 563
<212> PRT
<213> Homo sapiens

<400> 33

Met Ile Lys Arg Arg Ala His Pro Gly Ala Gly Gly Asp Arg Thr Arg
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Pro Arg Arg Arg Arg Ser Thr Glu Ser Trp Ile Glu Arg Cys Leu Asn
20 25 30

Glu Ser Glu Asn Lys Arg Tyr Ser Ser His Thr Ser Leu Gly Asn Val
35 40 45

Ser Asn Asp Glu Asn Glu Glu Lys Glu Asn Asn Arg Ala Ser Lys Pro
50 55 60

His Ser Thr Pro Ala Thr Leu Gln Trp Leu Glu Glu Asn Tyr Glu Ile
65 70 75 80

Ala Glu Gly Val Cys Ile Pro Arg Ser Ala Leu Tyr Met His Tyr Leu
85 90 95

Asp Phe Cys Glu Lys Asn Asp Thr Gln Pro Val Asn Ala Ala Ser Phe
100 105 110

Gly Lys Ile Ile Arg Gln Gln Phe Pro Gln Leu Thr Thr Arg Arg Leu
115 120 125

Gly Thr Arg Gly Gln Ser Lys Tyr His Tyr Tyr Gly Ile Ala Val Lys
130 135 140

1005463 01200

Glu Ser Ser Gln Tyr Tyr Asp Val Met Tyr Ser Lys Lys Gly Ala Ala
145 150 155 160

Trp Val Ser Glu Thr Gly Lys Lys Glu Val Ser Lys Gln Thr Val Ala
165 170 175

Tyr Ser Pro Arg Ser Lys Leu Gly Thr Leu Leu Pro Glu Phe Pro Asn
180 185 190

Val Lys Asp Leu Asn Leu Pro Ala Ser Leu Pro Glu Glu Lys Val Ser
195 200 205

Thr Phe Ile Met Met Tyr Arg Thr His Cys Gln Arg Ile Leu Asp Thr
210 215 220

Val Ile Arg Ala Asn Phe Asp Glu Val Gln Ser Phe Leu Leu His Phe
225 230 235 240

Trp Gln Gly Met Pro Pro His Met Leu Pro Val Leu Gly Ser Ser Thr
245 250 255

Val Val Asn Ile Val Gly Val Cys Asp Ser Ile Leu Tyr Lys Ala Ile
260 265 270

Ser Gly Val Leu Met Pro Thr Val Leu Gln Ala Leu Pro Asp Ser Leu
275 280 285

Thr Gln Val Ile Arg Lys Phe Ala Lys Gln Leu Asp Glu Trp Leu Lys
290 295 300

Val Ala Leu His Asp Leu Pro Glu Asn Leu Arg Asn Ile Lys Phe Glu
305 310 315 320

Leu Ser Arg Arg Phe Ser Gln Ile Leu Arg Arg Gln Thr Ser Leu Asn
325 330 335

His Leu Cys Gln Ala Ser Arg Thr Val Ile His Ser Ala Asp Ile Thr
340 345 350

Phe Gln Met Leu Glu Asp Trp Arg Asn Val Asp Leu Asn Ser Ile Thr
355 360 365

Lys Gln Thr Leu Tyr Thr Met Glu Asp Ser Arg Asp Glu His Arg Lys
370 375 380

1005463 01200

Leu Ile Thr Gln Leu Tyr Gln Glu Phe Asp His Leu Leu Glu Glu Gln
385 390 395 400

Ser Pro Ile Glu Ser Tyr Ile Glu Trp Leu Asp Thr Met Val Asp Arg
405 410 415

Cys Val Val Lys Val Ala Ala Lys Arg Gln Gly Ser Leu Lys Lys Val
420 425 430

Ala Gln Gln Phe Leu Leu Met Trp Ser Cys Phe Gly Thr Arg Val Ile
435 440 445

Arg Asp Met Thr Leu His Ser Ala Pro Ser Phe Gly Ser Phe His Leu
450 455 460

Ile His Leu Met Phe Asp Asp Tyr Val Leu Tyr Leu Leu Glu Ser Leu
465 470 475 480

His Cys Gln Glu Arg Ala Asn Glu Leu Met Arg Ala Met Lys Gly Glu
485 490 495

Gly Ser Thr Ala Glu Val Arg Glu Glu Ile Ile Leu Thr Glu Ala Ala
500 505 510

Ala Pro Thr Pro Ser Pro Val Pro Ser Phe Ser Pro Ala Lys Ser Ala
515 520 525

Thr Ser Val Glu Val Pro Pro Pro Ser Ser Pro Val Ser Asn Pro Ser
530 535 540

Pro Glu Tyr Thr Gly Leu Ser Thr Thr Gly Asn Gly Lys Ser Phe Lys
545 550 555 560

Asn Phe Gly

<210> 34
<211> 558
<212> DNA
<213> Homo sapiens

<400> 34
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ttcagaagag attccagaag gagcagaata tgatgatatg tgggatgtta gagaaatccc 180

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agagtatgag attatattca gacagcaggt gggaactgaa gatatatattt tagggttgtc 240
 aaaaaaggac tcctcaacag gttgttgacg tgaactagtg gctaaaatta aattgccaaa 300
 tacaaaccct tctgatattc aaattgatat ccaggaaaca atccttgacc ttcgtactcc 360
 tcagaagaag ctgttgataa ctcttcctga gctgggtggaa tgtaccagtg ccaaagcatt 420
 ctatatccca gagactgaaa ctcttgaaat ccctatgact atgaaaagag agttagatat 480
 tgctaatttc ttctgaaact gcatgaaaaa gataaaaagt agtaaaatgg cattggtaac 540
 aataaaaaaa ctttgaaa 558

<210> 35
 <211> 164
 <212> PRT
 <213> Homo sapiens

<400> 35

Gln Thr Asn Gly Leu Ser Thr Ile Gly Ala Met Gly Pro Gly Asn Ile
 1 5 10 15

Gly Pro Pro Gln Ile Glu Glu Leu Lys Val Ile Pro Glu Thr Ser Glu
 20 25 30

Glu Asn Asn Glu Asp Ile Trp Asn Ser Glu Glu Ile Pro Glu Gly Ala
 35 40 45

Glu Tyr Asp Asp Met Trp Asp Val Arg Glu Ile Pro Glu Tyr Glu Ile
 50 55 60

Ile Phe Arg Gln Gln Val Gly Thr Glu Asp Ile Phe Leu Gly Leu Ser
 65 70 75 80

Lys Lys Asp Ser Ser Thr Gly Cys Cys Ser Glu Leu Val Ala Lys Ile
 85 90 95

Lys Leu Pro Asn Thr Asn Pro Ser Asp Ile Gln Ile Asp Ile Gln Glu
 100 105 110

Thr Ile Leu Asp Leu Arg Thr Pro Gln Lys Lys Leu Leu Ile Thr Leu
 115 120 125

Pro Glu Leu Val Glu Cys Thr Ser Ala Lys Ala Phe Tyr Ile Pro Glu
 130 135 140

Thr Glu Thr Leu Glu Ile Pro Met Thr Met Lys Arg Glu Leu Asp Ile

100459 0120

145

150

155

160

Ala Asn Phe Phe

<210> 36
<211> 538
<212> DNA
<213> Homo sapiens

<400> 36
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agggacgcgg gaagagacca tgtgtgggaa atatgagtga gcatgtgaga acaagatccc 120
aatcctcaga aagaggaaat gaccaagagt cttcccagcc agttggatct gtgattgtcc 180
aggagcccac tgaggaaaaa cgtcaagaag aggaaccacc aactgataat cagggtattg 240
cacctagtgg ggagatcgaa aatgaaggag cacctgccgt tcaagggcct gacatggaag 300
cttttcaaca ggaactggct ctgcttaaga tagaggatga gcctggagat ggtcctgatg 360
tcagggaggg gattatgccc acttttgatc tctactaaagt gctggaagca ggtgatgcgc 420
aaccataggt ttcaagcaag acaaataag actgaaacca agaacgttat tcttaatctg 480
gaaatttgac tgataatatt ctcttaataa agttttaagt tttctgcaaa gaaaaaaaa 538

<210> 37
<211> 111
<212> PRT
<213> Homo sapiens

<400> 37

Met Ser Glu His Val Arg Thr Arg Ser Gln Ser Ser Glu Arg Gly Asn
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Asp Gln Glu Ser Ser Gln Pro Val Gly Ser Val Ile Val Gln Glu Pro
20 25 30

Thr Glu Glu Lys Arg Gln Glu Glu Glu Pro Pro Thr Asp Asn Gln Gly
35 40 45

Ile Ala Pro Ser Gly Glu Ile Glu Asn Glu Gly Ala Pro Ala Val Gln
50 55 60

Gly Pro Asp Met Glu Ala Phe Gln Gln Glu Leu Ala Leu Leu Lys Ile
65 70 75 80

Glu Asp Glu Pro Gly Asp Gly Pro Asp Val Arg Glu Gly Ile Met Pro
85 90 95

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Thr	Phe	Asp	Leu	Thr	Lys	Val	Leu	Glu	Ala	Gly	Asp	Ala	Gln	Pro
			100					105					110	

1005453 01220
2022.0 2345007